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OM protein - protein search, using sw model

Run on: August 22, 2003, 15:02:23 ; Search time 29 Seconds
(without alignments)
510.648 Million cell updates/sec

Title: US-09-745-506-37
Perfect score: 1799
Sequence: 1 MDKALISLNDPASTLFAE.....LEKNITILSTDRDLQVY 350

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Issued_Patents_AA:*
1: /cgn2_6/prodata/1/1aa/5A_COMB.pep:*
2: /cgn2_6/prodata/1/1aa/5B_COMB.pep:*
3: /cgn2_6/prodata/1/1aa/6A_COMB.pep:*
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5: /cgn2_6/prodata/1/1aa/PCFUS_COMB.pep:*
6: /cgn2_6/prodata/1/1aa/backfillsl.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	320.5	17.8	378	4	US-09-107-532A-4742 Sequence 4742, Ap
2	305	17.0	367	4	US-09-134-001C-3678 Sequence 3678, Ap
3	106	5.9	256	4	US-09-252-991A-24651 Sequence 24651, A
4	102	5.7	262	4	US-09-328-352-4482 Sequence 4482, Ap
5	101	5.6	673	4	US-09-146-053-2 Sequence 2, Appl
6	97.5	5.4	493	4	US-09-252-991A-28680 Sequence 28680, A
7	96.5	5.4	493	4	US-10-002-593-10 Sequence 10, Appl
8	96.5	5.4	588	4	US-09-328-352-7994 Sequence 7994, Ap
9	94.5	5.3	251	4	US-09-198-452A-156 Sequence 156, App
10	92	5.1	804	4	US-09-134-001C-5218 Sequence 5218, Ap
11	91	5.1	735	4	US-09-134-001C-3440 Sequence 3440, Ap
12	90	5.0	595	4	US-09-328-352-4432 Sequence 4432, Ap
13	90	5.0	1058	4	US-09-328-352-4276 Sequence 4276, Ap
14	89.5	5.0	2512	2	US-08-801-263A-9 Sequence 9, Appl
15	89.5	5.0	2512	3	US-09-102-248-9 Sequence 9, Appl
16	89.5	5.0	2512	4	US-09-367-764-9 Sequence 9, Appl
17	88.5	4.9	498	2	US-08-702-598-2 Sequence 2, Appl
18	88.5	4.9	800	3	US-08-776-265-3 Sequence 3, Appl
19	87.5	4.9	355	4	US-09-134-001C-5391 Sequence 5391, Ap
20	87	4.8	490	4	US-09-252-991A-18962 Sequence 18962, A
21	86.5	4.8	498	3	US-09-134-607A-19 Sequence 19, Appl
22	86	4.8	514	4	US-09-328-352-6997 Sequence 6997, Ap
23	86	4.8	729	4	US-08-887-534A-30 Sequence 30, Appl
24	86	4.8	729	4	US-09-527-431-30 Sequence 30, Appl
25	86	4.8	911	3	US-09-356-952-6 Sequence 6, Appl
26	85.5	4.8	1116	4	US-09-252-991A-32442 Sequence 32442, A
27	85	4.7	395	1	US-07-931-943-5 Sequence 5, Appl

28	85	4.7	837	2	US-08-680-326-117 Sequence 117, App
29	84.5	4.7	501	2	US-08-577-492-40 Sequence 40, Appl
30	84.5	4.7	501	3	US-09-079-630-40 Sequence 40, Appl
31	84.5	4.7	701	4	US-09-252-991A-23288 Sequence 23288, A
32	84	4.7	412	2	US-08-463-081B-14 Sequence 14, Appl
33	84	4.7	412	2	US-08-461-379A-14 Sequence 14, Appl
34	84	4.7	412	2	US-08-462-390B-14 Sequence 14, Appl
35	84	4.7	412	3	US-08-463-074B-14 Sequence 14, Appl
36	84	4.7	412	3	US-08-465-585C-14 Sequence 14, Appl
37	84	4.7	412	3	US-08-462-446-14 Sequence 14, Appl
38	84	4.7	412	4	US-09-462-624-2 Sequence 2, Appl
39	83.5	4.6	481	1	US-08-286-856C-2 Sequence 2, Appl
40	83.5	4.6	481	1	US-08-472-831-2 Sequence 2, Appl
41	83.5	4.6	498	4	US-09-328-352-7983 Sequence 7983, Ap
42	83.5	4.6	506	1	US-08-286-856C-3 Sequence 3, Appl
43	83.5	4.6	506	1	US-08-472-831-3 Sequence 3, Appl
44	83	4.6	599	3	US-09-080-983-9 Sequence 9, Appl
45	82.5	4.6	389	2	US-08-820-170A-13 Sequence 13, Appl

ALIGNMENTS

RESULT 1
US-09-107-532A-4742
Sequence 4742, Application US/09107532A
Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS: GENOME THERAPEUTICS CORPORATION
ADDRESS: 100 Beaver Street
City: Waltham
STATE: Massachusetts
COUNTRY: USA
ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD-ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Arliniello, Pamela Deneka
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 4742:
SEQUENCE CHARACTERISTICS:
LENGTH: 378 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium
FEATURE:
NAME/KEY: misc.feature
LOCATION: (B) LOCATION 1...378
SEQUENCE DESCRIPTION: SEQ ID NO: 4742:
US-09-107-532A-4742

Query Match 17.8%; Score 320.5; DB 4; Length 378;
Best Local Similarity 25.2%; Pred. No. 1.le-24;
Matches 100; Conservative 80; Mismatches 134; Indels 83; Gaps 16;

4 KALLSLNDFASLSFAESMDNVGL-----LVESPSPHNTLFLNDLLEEVEYLQAKA 59
11 RTFQKEESTYCPOMLAERGDVGLHIGLQK-----IQVMATLDVRAPEVEERAIKKI 65
QY 60 DLILSHPPPIPRPKRITNTWKERLYRALENVGIYSPTAYDAAPQGVNNMLAKGLG 119
DB 66 DLLIAKHPIPRPKRILVTDQPOEKMYADLLKHIDIAVYAATNMIDINDMNCCELLG 125
QY 120 -----ACTSRPIPRSKAPNPTTEGNHREVENNTQDLDVMSAVG-----IDGVSVT 168
DB 126 IEVSYLVKTHETIHYKLAAY-----VPVHAQMKREVLAAAGAGTGDYTGYSFT 176
QY 169 SFS-----ARTNEOTRINLCTOKALMQVDFLSRNOLYKT----- 208
DB 177 SIGGRFPPEAGAPAIKGVKTEQ-----VQEAKEVILPETIEKQVIOAMRSAPY 229
QY 209 -----EILSLERPLLHTGMRLCTLDESVALTMIDRIKRLKLSHRLALGVRTLES 263
DB 230 EEPAYDLFAIDEPYEMF-GLRGVGLPQEIFLEAFVEQVKAFAQLDGLRIY--GPKNAKS 286
QY 264 QKVVAALCAGSSSVL-OGV--EADLYLTGEMSHHDTLDAASQGINV-----LGEH 312
DB 287 SKKIALICGSGGKFFYPALQADVYTTGDIYTHAHDMQASGLAIDPGHYTESLCKQ 346
QY 313 SNTERGFLSDRLMDLSHLEN-KINILSETDRDPLQ 348
DB 347 RFIEK-FESMKQE-----ENMNDINFVSEINTNPFQ 376

RESULT 2
US-09-134-001C-3678
; Sequence 3678, Application US/09134001C
; Patent No. 6380370
; ORGANISM: Staphylococcus epidermidis
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 3678
; LENGTH: 367
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-3678

Query Match 17.0%; Score 305; DB 4; Length 367;
Best Local Similarity 24.3%; Pred. No. 4.2e-23;
Matches 96; Conservative 76; Mismatches 145; Indels 78; Gaps 13;

1 MDKALLSLNDFASLSFAESMDNVGLVPEPSPHTVNTLFLNDLLEEVEYLQAKAD 60
DB 2 MKISLMEVLNNHVFHQAESMDNVGLI-GNDKLDIGILTLTDDCTDDVQAIAELNTN 60
QY 61 LILSYHPPIPRPKRITNTWKERLYRALENVGIYSPTAYDAAPQGVNNMLAKGLG 120
DB 61 TLIAHHPPIPRPKRITNTWKERLYRALENVGIYSPTAYDAAPQGVNNMLAKGLG 119
QY 121 CTSRPIPRSKAPNPT-----EGHRYEF-----NVNTQ 150
DB 120 ENISMINTNSSYYKYQTFIPKNTYIEDKDSLNLGLAKEGYECFESSEKGGFGPVG 179
QY 151 DLDKMSAVKIDGVSYSFSARTGNEGTIRINLCTOKALMQ-----VYDFLSRNQ 203

DB 180 DASPYIGLDSIEYVDKELEFMKDNF-----LEIRKALIDNHNPETPYFDDIKANKE 234
QY 204 LYOKTEILSLERPLLHTGMRLCTLDESVALTMIDRIKRLKLSHRLALGVRTLES 263
DB 225 -----SEVGLIGIQLOTMTLDERSEYAKKOLNIPSVRY---TGOH-DS 275
QY 264 QKVVAALCAGSSSVLQGE-----ADLYLTGEMSHHDTLDAASQGINVILCEHSNTE 316
DB 276 PIKRVAILIGSGSI-----GFEYKASQLGADVTVTGDIKHDAIDAKIQNVNLLDINH-YSE 330
QY 317 RGLSLDRLMDLSHL---ENKINITSETDRDPLQ 348
DB 331 YMKEGLEKLEKMLFKYENQPIYASINDPDK 365

RESULT 3
US-09-252-991A-24651
; Sequence 24651, Application US/09252991A
; Patent No. 6551795
; ORGANISM: Pseudomonas aeruginosa
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 24651
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-24651

Query Match 5.9%; Score 106; DB 4; Length 256;
Best Local Similarity 19.1%; Pred. No. 0.01; Mismatches 124; Indels 102; Gaps 9;

3 KALLSLNDFASLSFAESMDNVGLVPEPSPHTVNTLFLNDLLEEVEYLQAKADLI 62
DB 9 LSTLVEADRYLDARIDYCPNGLOVGRP--QVRRIYSGTASQALLDAVEADADV 66
QY 63 LSYHPPIPRPKRITNTWKERLYRALENVGIYSPTAYDAAPQGVNNMLAKGLGAC 121
DB 67 LVNHGVPKGENPCVVG-MKQRLKTLNNDISLALYHLPDLHPEVGNNOVLARQLGE 125
QY 122 TSPRIHPSKAPNPTTEGNHREVENNTQDLDKMSAVKIDGVSVTSPSARTGNEGT 181
DB 126 VEGPLEP-----GNR-----S 137
QY 182 ININLCTOKALMQVDFLSRNOLYOKTEILSLERPLLHTGMRLCTLDESVALTMIDR 241
DB 138 IYLLSLSAEPMPAPAFARHVRDALGR-----EPLVDAG----- 171
QY 242 IRRHLKLSHRLALGVRTLESQKVVAALCAGSSSVL-QGYEA--DLYLTGEMSHHDTL 298
DB 172 -----OPIRRIAMCTGAGGYDQAIAGADVALTGEVSEQTVA 210
QY 299 DAASQGINVILCEHSNTERGFLSDRLMDL 327
DB 211 SARENGISFTIAGHATERYGVALGDYL 239

RESULT 4
US-09-328-352-4482
; Sequence 4482, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.

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; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE OF INVENTION: BAUMANNI FOR DIAGNOSTICS AND THERAPEUTICS
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 4482
; LENGTH: 262
; TYPE: PRN
; ORGANISM: Acinetobacter baumannii
US-09-328-352-4482

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Query Match      5.7%; Score 102; DB 4; Length 262;
Best Local Similarity 18.3%; Pred. No. 0.028;
Matches 62; Conservative 39; Mismatches 105; Indels 132; Gaps 13;

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QY 6 LLSLNDFAASLSFAESW-DNV-----GLLVESPPHTVTLFLNDLLEVM 52
DB 4 LNSGNIMANLHEIIOCMQDTLKAEFKDYAPRGLQEGST--EVKRIICNVASEDAID 61
QY 53 EYLQKKAADLLSYHPPIFR---PMKRITMTWKELVIRALENRGYSPTAYDAAPQ 108
DB 62 AAIKADADLLVHGHTFMGEPYITGMGNRIK---KLIONNISTLAVHLPDAPHS 116
QY 109 -GVNNMLAKGLACTSRPI-----HPSKAPNYPEEGNHRYEFVNTQDLKMSAVKGI 162
DB 117 LGNNIIMAKKLNQNLNLEPIDLTEKHPIG-----NIGILE----- 150
QY 163 DGVSATSFARKTNEQOTRINLNCIOKALMOVVDPLSRNKOLYOKTEIISLEKPLLIHTG 222
DB 151 QALSYEEFKAK-----LQNGFDK---KVHLPKESQSIQK----- 182
QY 223 MGRILTLDESVSATMIDRIKRLKLSHRLAAGVRTLESQKVAALCAGSSSVLYQGV 282
DB 183 -----VGFCTGGAQDFIATA 197
QY 283 ---EADLYLTGEMSHHDTLDAASQGINVILCEHSNTER 317
DB 198 ALQNCDAVYISGEVSERTFEAKELSVHYFACGHNAER 235

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RESULT 5
US-09-146-053-2
; Sequence 2, Application US/09146053A
; Patent No. 6399349
; GENERAL INFORMATION:
; APPLICANT: Ryan, James W.
; APPLICANT: Sprinkle, Terry Joe Curtis
; APPLICANT: Venema, Richard C.
; TITLE OF INVENTION: Human Amino peptidase P Gene
; FILE REFERENCE: MCG103
; CURRENT APPLICATION NUMBER: US/09/146,053A
; CURRENT FILING DATE: 1998-09-02
; EARLIER APPLICATION NUMBER: 60/057,854
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 673
; TYPE: PRN
; ORGANISM: Homo sapiens
US-09-146-053-2

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Query Match      5.6%; Score 101; DB 4; Length 673;
Best Local Similarity 19.9%; Pred. No. 0.16;
Matches 70; Conservative 55; Mismatches 121; Indels 106; Gaps 16;

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QY 20 ESDNDNGLVESPPTVTLFLNDLLEVMEEVLQKADLLI-SYHP-----PIRPM 73
DB 164 DTWESYDLAQSNRLQVS---ITTNL-----VDLVGSRPVPVQPIYALQ 208
QY 74 KRITMTWKELVIRALENRGYSPTAYDAAPGV-----NMMLAKGLACTSRPI 126

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DB 209 EAFTGSMQEKV-----SGVRSQMOKHQKVPYAVLLSALEETAWLFN-----L 251
QY 127 HPSKAPNYPEEGNHRYEFVNTQDLKMSAVKGDVSVTSFSAFTGNEBOTRILNC 186
DB 252 RASDIPYNP-----FFYSYTLND-----SSIRLFANKSPFSSETLSYLSSC 294
QY 187 TOKALMOVDF-----LSRNKOLYOKTEIISLEKPLLIHTGMGRIC 228
DB 295 TGPACVQIEDYISOVRDIAQVSLGDVRIWIGTITMGIEMIPREK-----L 342
QY 229 LDESVSATMIDRIKRL-----KLSHIRLALGVGR--TLSESQKVAALCAGSSSVLQ 280
DB 343 VTDTYSPVMTKAVKNSKEQALAKASHVRDAVAVIRLVMLEKNVPRTGVDDESGAETVD 402
QY 281 GVEADLYLTGEMSHHDTLDAASQGINVILCEHSNTE---RGLSLDLMDIDS 329
DB 403 KFRGEQFSSGPS--FETISAS--GLNNAALAHYSPTELNRKLSDEMYLDS 451

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RESULT 6
US-09-252-991A-28680
; Sequence 28680, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 28680
; LENGTH: 509
; TYPE: PRN
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-28680

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Query Match      5.4%; Score 97.5; DB 4; Length 509;
Best Local Similarity 24.8%; Pred. No. 0.24;
Matches 52; Conservative 41; Mismatches 70; Indels 47; Gaps 12;

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QY 135 PTBSNHRVEFVNNTQDLKMSAVKGDVSVTSFSAFTGNEBOTRINLNCIOKALMOV 194
DB 199 PDG--RISLRVG--GREVDIRVSTLPBANGERRV--LRLLDKOAGRLNL-----OH 244
QY 195 VDLFSRKKOLYOKTEIISLEKPLLIHTGMGRICLT-----DESVSATMIDR 241
DB 245 LQMSERDKLMDT-----VAKPHGILLVGTGSGKTTILYASLTTLNDRIKRLIYEDP 300
QY 242 IKRHLKLSHRLAAGVRTLESQKVAALCAGSSSVLYQGVADLYLTGEMSHHDTLDA 300
DB 301 IEYHLE-----GIGOT---QVNAKVDMTFARGLAIRLRDPDVAVGEIRDRFAEI 349
QY 301 ASQ-----GINVILCEHSNTERGLSLDLMD 326
DB 350 AVOASLGHVLTSLHTNSAISGATIRLVDM 379

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RESULT 7
US-10-002-593-10
; Sequence 10, Application US/10002593
; Patent No. 6586198
; GENERAL INFORMATION:
; APPLICANT: Vanderbilt University
; APPLICANT: Brown, Nancy J.
; TITLE OF INVENTION: BIOLOGICAL MARKERS AND DIAGNOSTIC TESTS FOR ANGIOTENSIN CONVERTING ENZYME
; FILE REFERENCE: Atty Docket No. 6586198 1242/48/2
; CURRENT APPLICATION NUMBER: US/10/002,593

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ORGANISM: Staphylococcus epidermidis
US-09-134-001C-5218

Query Match 5.1%; Score 92; DB 4; Length 804;
Best Local Similarity 17.5%; Pred. No. 1.8;
Matches 67; Conservative 61; Mismatches 113; Indels 142; Gaps 15;

QY 8 SSLNDFAISLFAESMDNGLVE-----PSPPHTVN-TLFTNDLTGEVMEYLOK 57
DB 84 SSYVD-AMVRLSGDWLRLHVLLEMGNNSIDNDPPAAMRYTAKLSQSEELRDINKE 142
QY 58 KADLLISHPPIPRPKRTTWTNTERLVIRALENRYIS-----PHT----- 101
DB 143 TWSFIRNYDDTLEPM-----VLPAFPLLLINGSTGSSGYATDIPRNLAEVIQGT 196
QY 102 AVDAAPQVNNMLAKGLGACTSRPIHPSKAPNPTSGNHNHVEENVYTDLDKVMASVKG 161
DB 197 KYIDPDITINOLMKYI-----KGPDPFG-----ITOG 226
QY 162 IDGVS-----VTSFARTGNEE--QTRINLCTOKALMQVDFLSRNKOL 204
DB 227 IEGIKAVETGKGKVVVRSDVEPLRSGRKQLIVEIPEYVKKSLVKRIDELRADKK- 285
QY 205 YOKTEILSLKPLLTGMRCLCTDESYSLATMDIRKRLKLSHRLALGVGRLESQ 264
DB 286 -----VDGIYEVRDETR-----TGLRIAELEKRDANS- 313
QY 265 VKVVALCAGSSVLOGVADLYLJGEM--SHHDTLDASOGINVLCEHSNTERGLSD 322
DB 314 -----ESIKNYLYKNSDLQISTYFNVAALSEG-----RPLMG 346
QY 323 LRDMDSHLENKINIILSETDRD 345
DB 347 LRRIESYLNHQIEVVTNRTRYD 369

RESULT 11
US-09-134-001C-3440

Sequence 3440, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 3440
LENGTH: 735
TYPE: PRT
ORGANISM: Staphylococcus epidermidis
US-09-134-001C-3440

Query Match 5.1%; Score 91; DB 4; Length 735;
Best Local Similarity 20.7%; Pred. No. 2;
Matches 86; Conservative 58; Mismatches 161; Indels 110; Gaps 17;

QY 16 LSFAESMDNGLVLEPSPPHTVNTLFTLNDLPEVMEYLOKADLLSHPPPIR--PM 73
DB 319 MAFSETEQSMVLVEGTQOKFLDLFNKHELSAVGEVTDIDR-FVLYTDEVDYDIPV 377
QY 74 KRIT-----NTWK-----ERLVIRALENRYISPTAYDAPO--G 109
DB 378 QPLADAPYLLIEGEKEKNTSKNDYSNIDVHTFKLLQHP-ISKHHLYVQYDQOYG 436
QY 110 VNNMLAKGLGACTSRPIHPSKAPNPTSGNHNHVEENVYTDLDKVMASVKGIDGVSVTS 169
DB 437 ANTIIRKGLQASVVRVEGTOKAIASTIDEARVFNQPEGKMYVAEAVRNLLAVGAP 496

QY 170 FS-----ARGNEBOTRI--NLNCTOKALMQVDFL-----SRNKOYOKTEILS----- 212
DB 497 LAITDCLNLTGSPKKEIYQOLIDSTKMSACKVLOTPIVSGVSLNTRGTSIPPTPV 556
QY 213 -----LEKPLLLHTGMG--RLCTIDE 231
DB 557 VGMVGLIEDVSYLKEFKPKAGDKIYVGETRDDPGGSQLEK--LVGSVNHEFESIDLD 614
QY 232 SVSLATMDIRKRLKLSHRLALGVGRLESQYKVALCAGSSVLOGVADLYTGE 291
DB 615 EVSKRKLKQALIRNGIASHQ--TVGKGGLLYTLAKISA-----HYDLQAOQDLDTNA 666
QY 292 MSHHDTLDASOGINVLCEHSNT-----ERGFIS--DLRMDLSHLENKINI 337
DB 667 QLTSER-----QGRIVYVVEGQTLDDIDQAEIGHLTHQOLFDSNDVAKIKENV 716

RESULT 12

US-09-328-352-4432
Sequence 4432, Application US/09328352
Patent No. 6562958

GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTE
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 4432
LENGTH: 595
TYPE: PRT
ORGANISM: Acinetobacter baumannii
US-09-328-352-4432

Query Match 5.0%; Score 90; DB 4; Length 595;
Best Local Similarity 20.1%; Pred. No. 1.8;
Matches 54; Conservative 45; Mismatches 95; Indels 74; Gaps 11;

QY 112 NMLAKGLACTSRPIHPSKAPNPTSGNHNHVEENV-----YQDDDKVMSAVKGI 162
DB 216 DWILOAFQESADIDHNE-----PRKNGCVRRRIDVLTITYNMPSNTLTAYSISRIKL 270
QY 163 DGVSYS-----FSARTGNEBOTRIINCT-----OKALQV--DFLSRNKO----- 203
DB 271 GRANAEKRRPQGRKLTPTPKGQETRLSTLPTAGEKLVARIIPDVLYNSFOOLGF 330
QY 204 -----LYOKTEILSLKPLLT--HTGMRCLCTL-----DESVSLATMDIRK----- 243
DB 331 DQSLQOWQRIITNSHGIILVTGPTGSKTTLTYSSLKQLATQVNVCTIEDPLEMPS 390
QY 244 -RHUKSHIRLAGVGTLESQYKVALCAGSSSVLOGVADLYLGESSHDT-----L 298
DB 391 FNMQOVNH-----AIEIGFADVRLALRDPDIIIMIGEIRDDTANMAI 434
QY 299 DAASOGINVLCEHSNTERGLSDLRDM 326
DB 435 QAAHLGHLVLTHTNDAPSSLTRLHDL 462

RESULT 13

US-09-328-352-4276
Sequence 4276, Application US/09328352
Patent No. 6562958

GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTE
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252

TELEFAX: 919-881-3175
 ; INFORMATION FOR SEQ ID NO: 9:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 2512 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-09-102-248-9

Query Match 5.0%; Score 89.5; DB 3; Length 2512;
 Best Local Similarity 18.6%; Pred. No. 21;
 Matches 71; Conservative 50; Mismatches 134; Indels 137; Gaps 15;

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QY 30 EPSPPHTVMTLEFLTNDLTEEYME-EVLQKKADLILSYHPPIFRPMKR-----ITWN 79
Db 1908 DPGPGHLQKKSVLQNLTEPLELERNLIER-----IHAVLDTSKEQLKRYQMMPTE 1960
QY 80 TWKERLVIRALENRVGISPHNAVDAPOGVNMLAKGLGACTS-----RPI 126
Db 1961 ANKSRYSQSRKVENOKAITTER-----LISGLRLVNSATDQPCYKITYPKPL 2007
QY 127 HPSKAP-----NPTPEGNHRVEFNVTODLDKMSAVKIDGVSV 167
Db 2008 YSSSVFANTSDPOFAVAVCNNTLHENYPTVASVQI--TDEYDAYILDMVDGFFVACLDTATP 2065
QY 168 TSFSARTGNNEO-----TRINLNCYOKALMQVVDFLSRN 201
Db 2066 CPAKLASYPKKHRYRAPNIRSAVPSAMQNTLQNVLIATYRNCNVTOMRCLPTLDSKTFN 2125
QY 202 KQLYOK-----TEILSL-----EKPILLHTGMGRCLTLDSEVSL 235
Db 2126 VECFRKYACNDEYEEFARKPIRITTEFVYAVARLKGPKAALFAKTYNLVPLQE-VPW 2184
QY 236 AFWIDRIKRIKLKLSHRLALGVGRILE-SQVKYVALCAGSGSSVLOGVEADLY--LTGEM 292
Db 2185 DRFVMDMKRDVAVTP-----GKHKTEERPRKVVQVIOAAEPLATAYLGGIHRRLVRLTAVL 2239
QY 293 --SHHDTLDAASQGINVILCEH 312
Db 2240 LPNRIHTLFDMSAEDFDALITAEH 2261

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Search completed: August 22, 2003, 15:07:27
 Job time : 31 secs

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